

Amendments to the Specification:

Please amend the specification as follows:

Please delete the paragraph on page 2, line 25 to page 3, line 7 and replace it with the following paragraph:

The domain structure of ADAMTS-13 has a signal peptide preceding a propeptide that ends in a RQRR (SEQ ID NO: 19) sequence as a furin cleavage motif, followed by a metalloprotease domain containing a reprotoxin-type zinc-chelating region consisting of HEXXHXXGXXHD (SEQ ID NO: 20) as a consensus sequence (to amino acid residue No. 284 (p285X)); via a disintegrin-like domain as found in snake venom metalloprotease (to amino acid residue No. 386 (W387X)), there exists a first Tspl motif (Tspl-1) consisting of approximately 50 to 60 residues generally considered to be important for molecular recognition (to amino acid residue No. 448 (Q449X)), which continues to a Cys-rich region containing a RGDS (SEQ ID NO: 21) sequence as one of cell adhesion motifs (to amino acid residue No. 580 (T581X)); and, through a spacer domain consisting of approximately 130 amino acid residues with no cysteine residue (to amino acid residue No. 687 (W688X)), additional Tspl motif repeats (Tspl-2 to Tspl-8) follow, which is followed by a CUB domain-1, and -2 that are said to be first found in a complement component C1r or C1s.